REMARKS

On pages 1 and 4 of the Office Action, the Examiner indicates that Claims 26 and 29-40 are pending, Claims 26, 29, 31-33, 35, 39 and 40 are rejected, and Claims Claim 30, 34 and 36-38 are objected to, but would be allowable if rewritten in independent form.

In paragraph 4, on page 3 of the Office Action, the Examiner rejects Claims 26, 29 and 40 under 35 U.S.C. § 102(b) as being anticipated by Médigue et al.

Specifically, the Examiner states that Médigue et al teaches a method of sequencing all or part of a target nucleic acid sequence, as recited in Claim 26, wherein the magnifying tags are the individual restriction sites of the *E. coli* chromosome restriction map.

For the following reasons, Applicant respectfully traverses the Examiner's rejection.

Medigue et al describes software which locates unknown DNA fragments from *E. coli* in an *E. coli* restriction map. The Examiner considers that the "magnifying tags" in Medigue et al are the individual restriction sites of the *E. coli* chromosome restriction map. However, these restriction enzyme sites do not "correspond to", i.e., are associated with, bases in the fragment being sequenced, they are the bases in the fragment being sequenced.

Accordingly, Applicant respectfully submits that the present invention is not taught or suggested in Medigue et al, and thus request withdrawal of the Examiner's rejection.

On page 4 of the Office Action, the Examiner rejects Claims 26, 29, 31-33, 35 and 39 under 35 U.S.C. § 102(b) as being anticipated by Shumaker et al.

Specifically, the Examiner states that Shumaker et al teaches a method of sequencing all of or part of a target nucleic acid molecule, wherein the magnifying tags are labels indicating which base is present and the positional maker is the sequence shown in Figure 3 thereof.

For the following reasons, Applicant respectfully traverses the Examiner's rejection.

It is submitted that the overlapping sequences in Figure 3 of Schumaker et al do not provide reference to a restriction map or a distinct "positional marker". A number of sequences are required to position each sequence relative to one another. In the method defined by the main claim, a single sequence can be positioned in the target polynucleotide by identifying a positional marker by reference to a restriction map.

Accordingly, Applicant respectfully submits that the present invention is not taught or suggested in Schumaker et al, and thus request withdrawal of the Examiner's rejection.

The method of the present invention allows the identification of a portion of a target nucleic acid molecule and the determination of the position of this portion, in a single method that requires only a single target nucleic acid molecule. In the method of Shumaker et al, to position each fragment, a plurality of fragments is required, as demonstrated by Figure 3. The repetition of sequencing events is not required by current Claim 26, where each identified portion is identifiable according to its position (determined by a

positioned marker or restriction map) within the target nucleic acid molecule. The claimed method is therefore advantageously more simple than the prior art methods, thereby providing an improved sequencing method that could not be predicted from the prior art.

In view of the amendments to the claims and the arguments set forth above, reexamination, reconsideration and allowance are respectfully requested.

The Examiner is invited to contact the undersigned at the below-listed number on any questions which might arise.

Respectfully submitted,

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